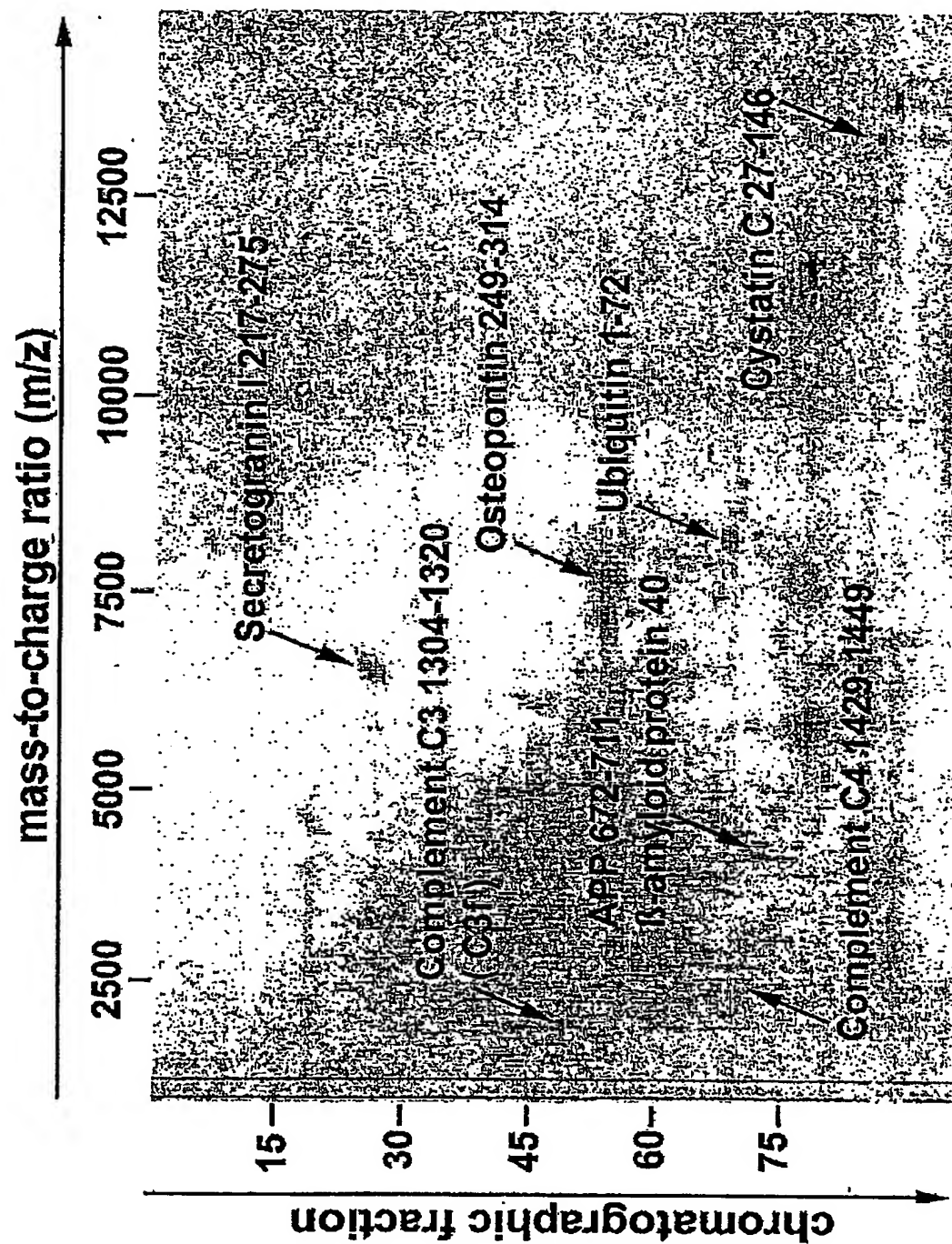
**Fig. 1**

**Fig. 2**

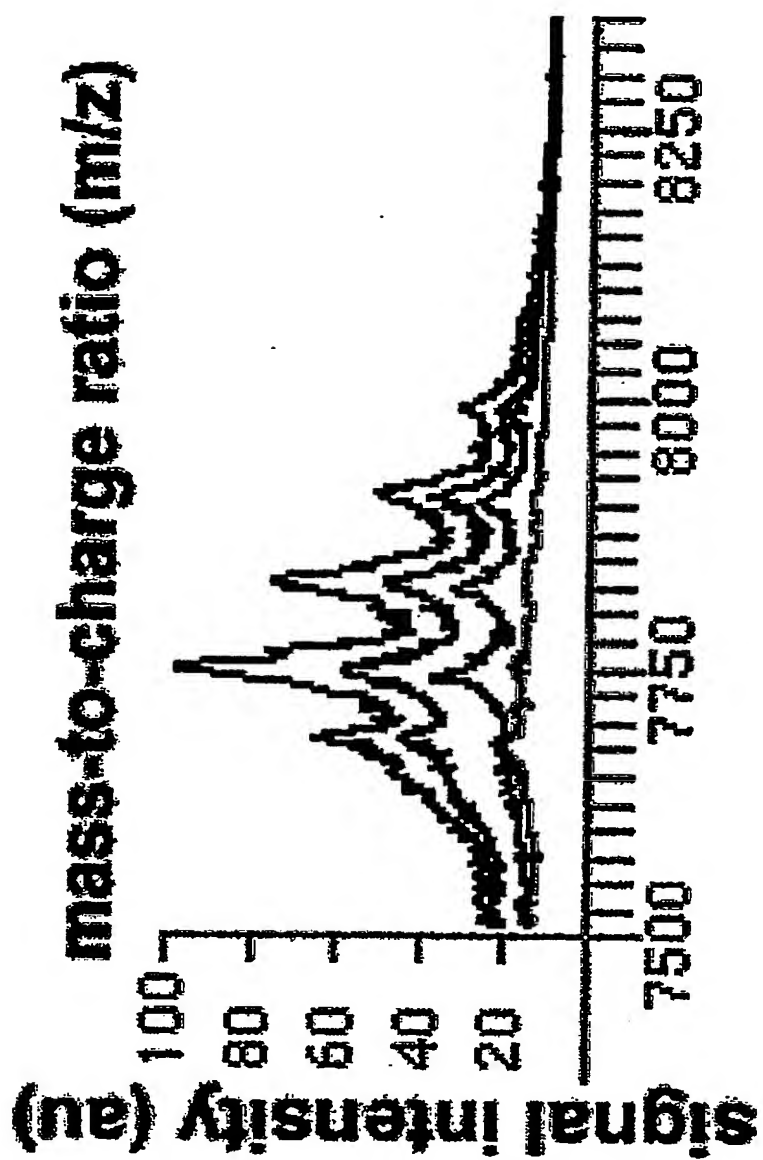
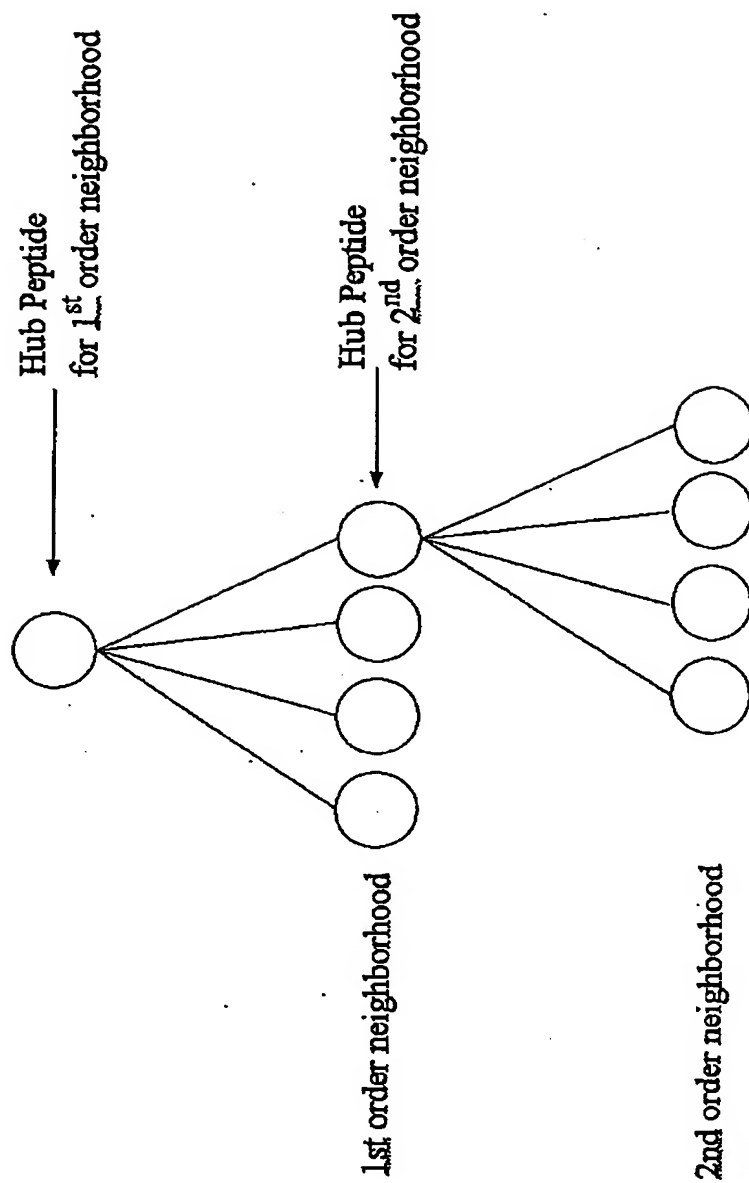
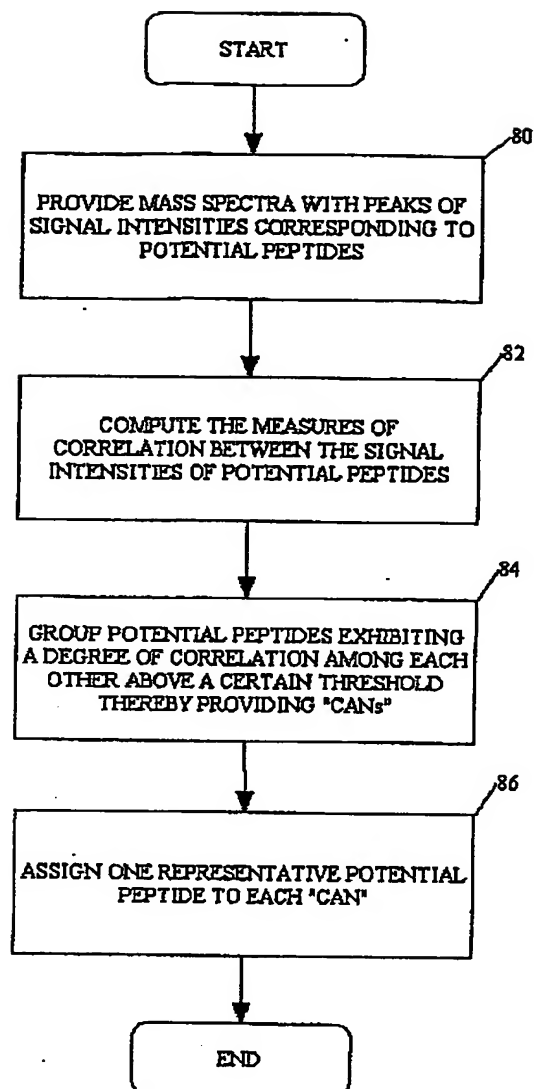
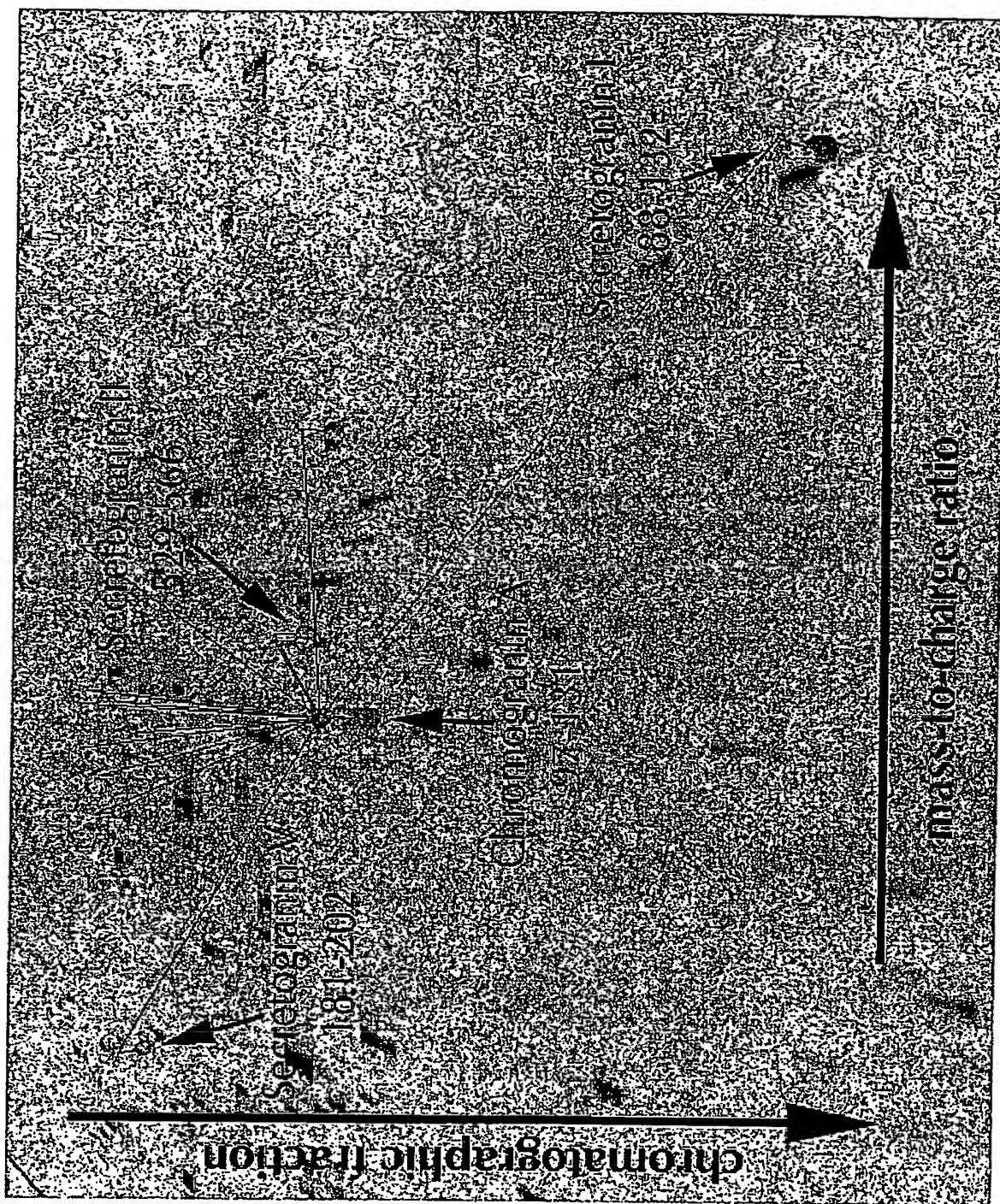
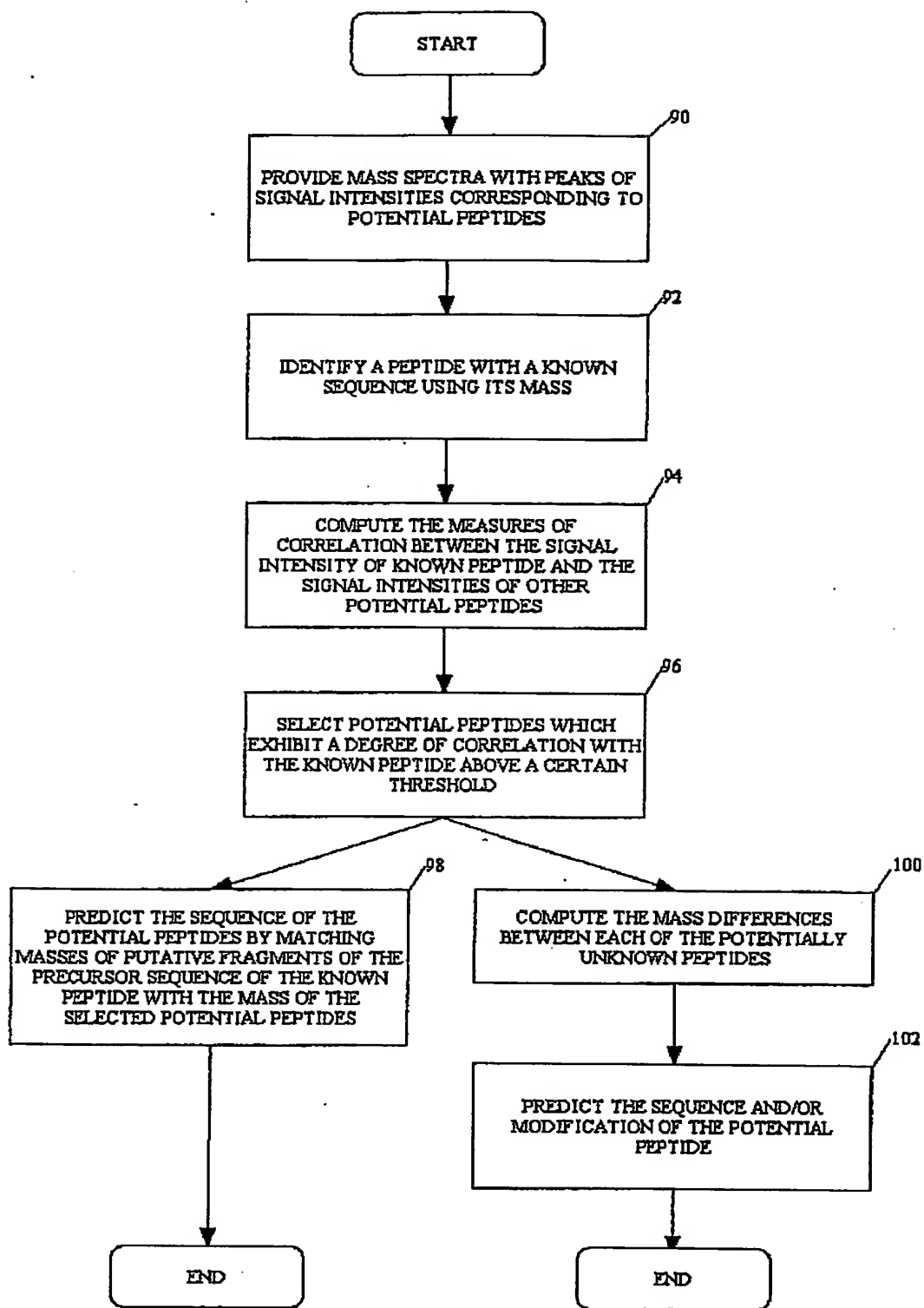


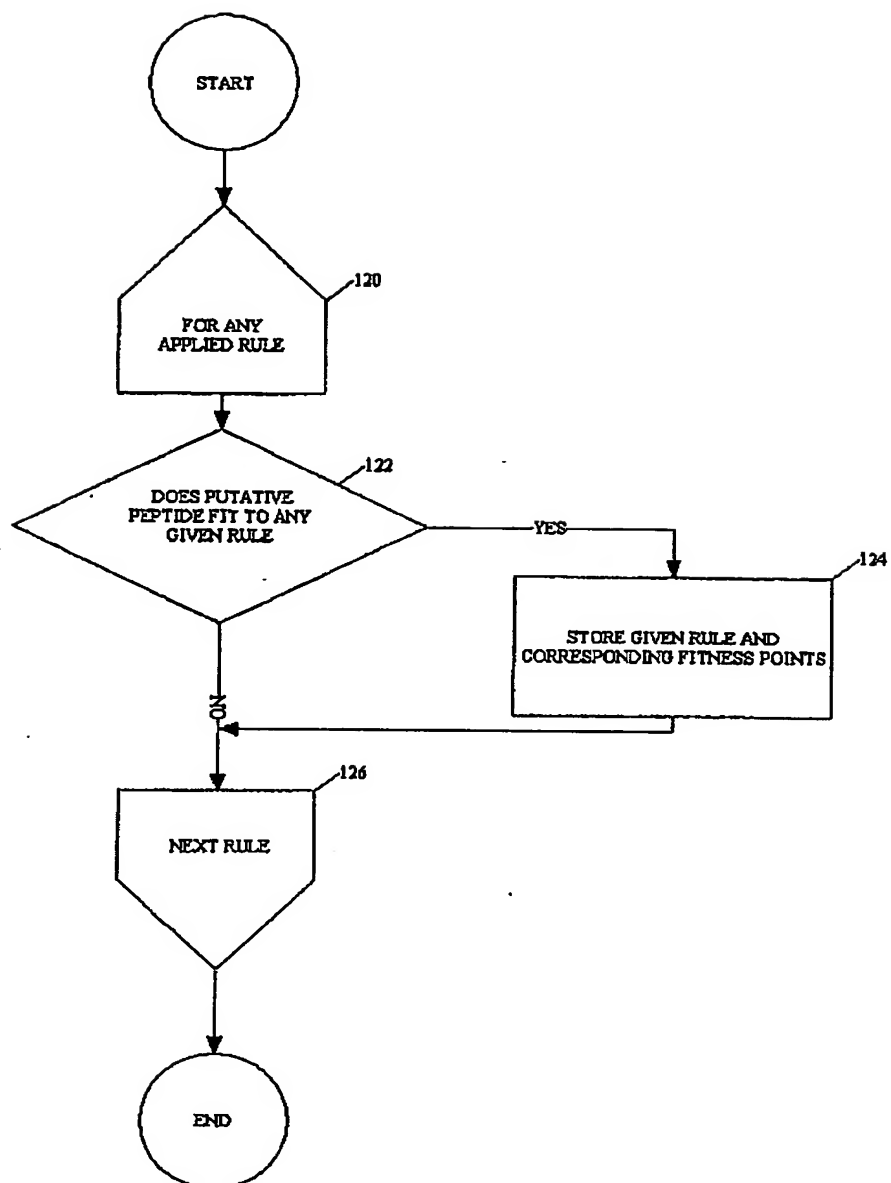
Fig. 3

**Fig. 4**

**Fig. 5**

**Fig. 6**

**Fig. 7**

**Fig. 8a**

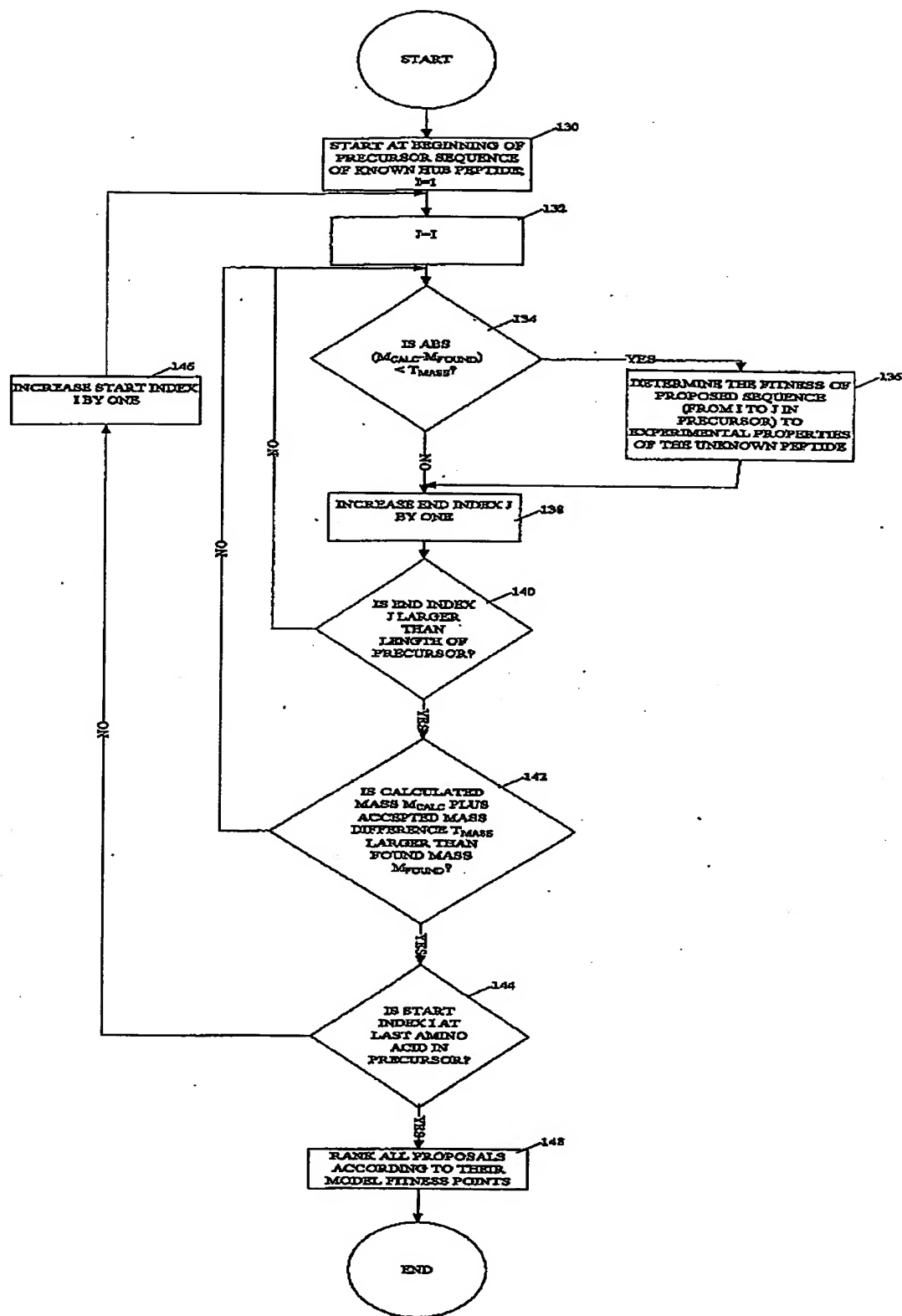
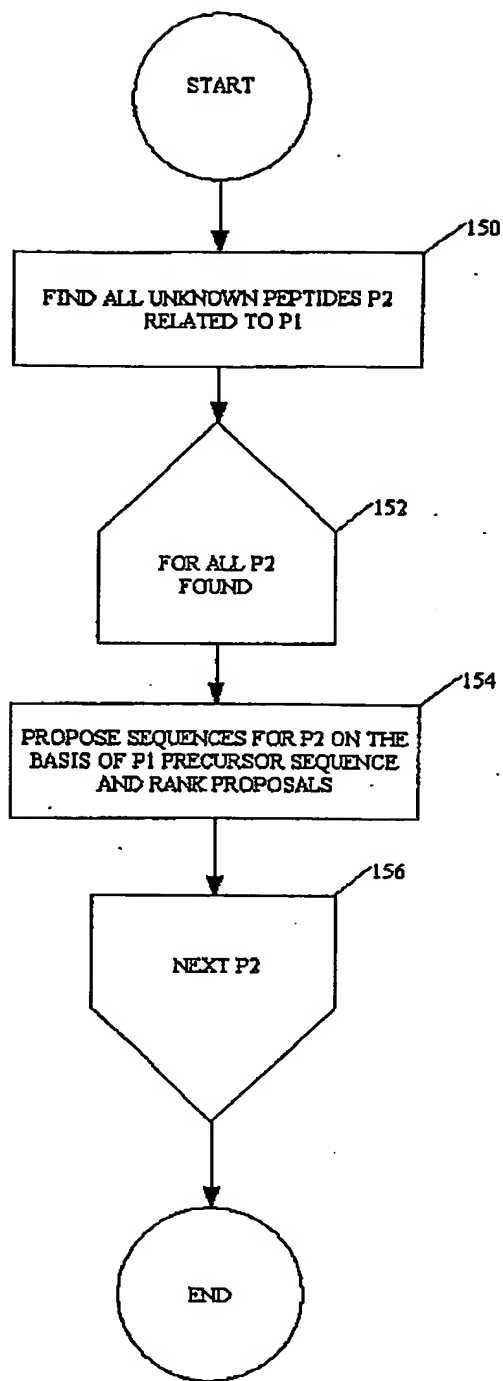
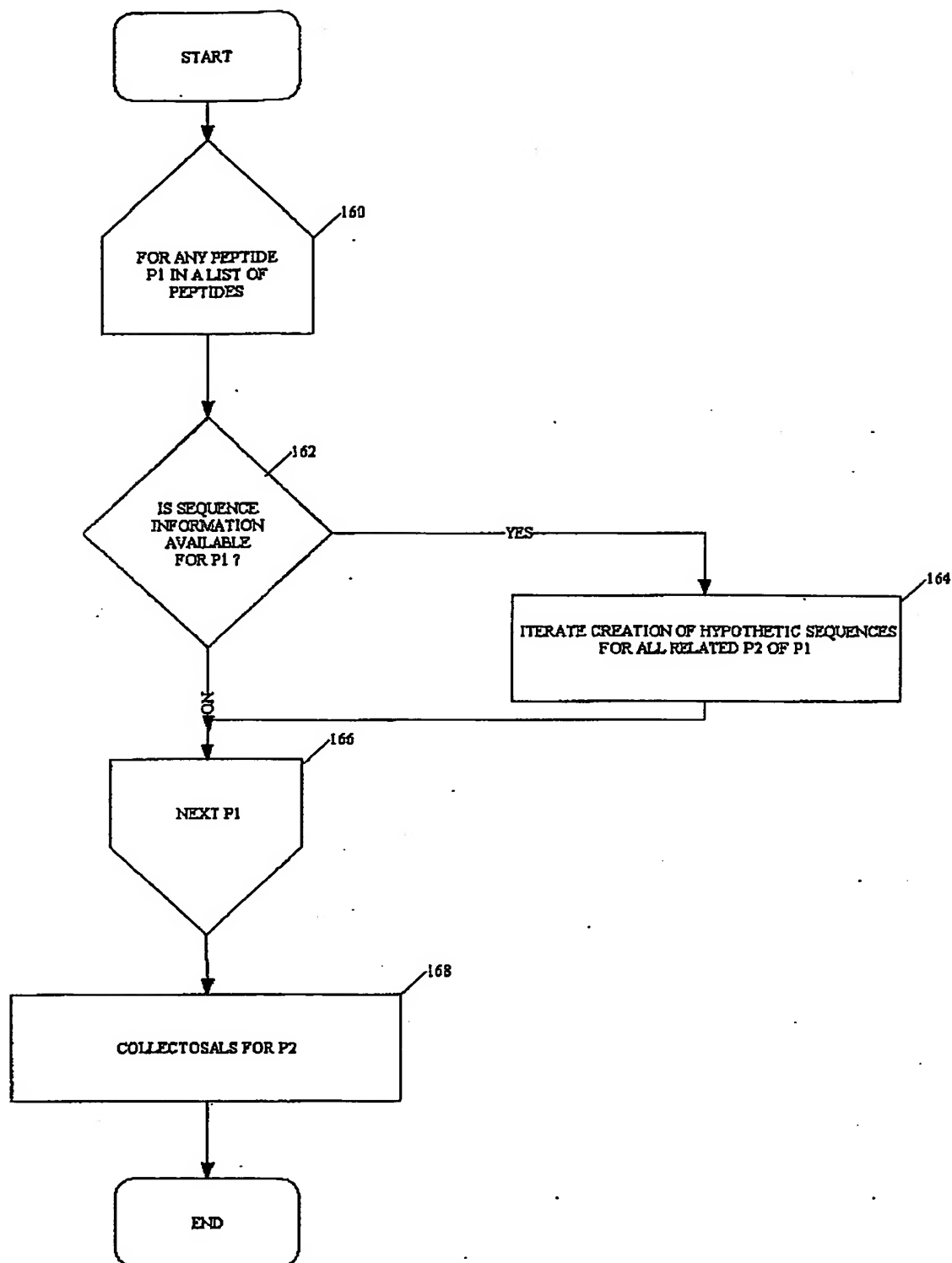


Fig. 8b

**Fig. 8c**

**Fig. 8d**

Modification	Monoisotopic Mass	Average Mass
4-Phosphoantethine	839.0780	839.8294
5-Adenylation	829.0525	829.2081
Acetylation	42.0106	42.0873
ADP-ribosylation (from NAD)	541.0611	541.8052
Biotinylation (amide bond to lysine)	226.0776	226.3994
Carboxylation of Asp and Glu	43.9898	44.0098
C-terminal amide formed from Gly	-0.9840	-0.9847
Cysteinylation	119.0041	119.1442
Deamidation of Asn and Gln	0.9840	0.9847
Deoxyhexoses (Fuc, Rha)	146.0579	146.1430
Disulphide bond formation	-2.0157	-2.0159
Farnesylation	204.1878	204.8556
Formylation	27.9949	28.0104
Ceramylation	272.2504	272.4741
Glutathionylation	305.0682	305.3117
Hexosamines (GalN, GlcN)	161.0688	161.1577
Hexoses (Fru, Gal, Glc, Man)	162.0528	162.1424
Homoserine formed from Met by CNBr treatment	-29.9928	-30.0835
Hydroxylation	15.9949	15.9994
Lipoic acid (amide bond to lysine)	188.0330	188.8147
Methylation	14.0157	14.0269
Myristoylation	210.1984	210.8598
N-acetylhexosamines (GalNAc, GlcNAc)	203.0794	203.1950
N-acetylneuraminic acid (Sialic acid, NeuAc, NANA, SA)	291.0954	291.2579
N-glycolylneuraminic acid (NeuGc)	307.0908	307.2573
Oxidation of Met	15.9949	15.9994
Palmitoylation	258.2297	258.4186
Pentoses (Ara, Rib, Xyl)	132.0428	132.1161
Phosphorylation	79.9663	79.9799
Proteolysis of a single peptide bond	18.0106	18.0159
Pyridoxal phosphate (Schiff Base formed to lysine)	231.0297	231.1449
Pyroglutamic acid formed from Gln	-17.0265	-17.0806
Stearoylation	266.2610	266.4674
Sulphation	79.9568	80.0642

Fig. 9

Motif	Enzyme/ Reaction	Mass difference(average mass)
W	photochemical	+16
W	photochemical	+32
W	photochemical	+4
[ST]-X-[RK]	Protein kinase C	+79.9799

Fig. 10

Symbols		Monoisotopic Mass	Average Mass
Gly	G	57.02146	57.05
Ala	A	71.03711	71.08
Ser	S	87.03202	87.08
Pro	P	97.05276	97.12
Val	V	99.06841	99.07
Thr	T	101.0476	101.1
Cys	C	103.0091	103.1
Leu	L	113.0840	113.2
Ile	I	113.0840	113.2
Asn	N	114.0429	114.1
Asp	D	115.0269	115.1
Gln	Q	128.0585	128.1
Lys	K	128.0949	128.2
Glu	E	129.0425	129.1
Met	M	131.0404	131.2
His	H	137.0589	137.1
Phe	F	147.0684	147.2
Arg	R	156.1011	156.2
Tyr	Y	163.0633	163.2
Trp	W	186.0793	186.2

Fig. 11

	Composition	Monoisotopic Mass	Average Mass
N-Terminal Groups			
Hydrogen	H	1.00782	1.0079
N-Formyl	HCO	29.00274	29.0183
N-Acetyl	CH ₃ CO	43.01839	43.0452
C-Terminal Groups			
Free acid	OH	17.00274	17.0073

Fig. 12

Additional Amino acid	+/- Fraction numbers
E, Glutamic acid	+ 0.47
F, Phenylalanine	+ 5.54
H, Histidine	- 3.82
I, Isoleucine	+ 2.86
K, Lysine	- 1.72
L, Leucine	+ 5.15
Q, Glutamine	- 0.85
S, Serine	- 0.45
V, Valine	+ 2.2
W, Tryptophane	+ 5.35
Y, Tyrosine	+ 2.92

Fig. 13

AminoAcid Before First Cleavage				
		% Cleavage	% Present	Δ
A	24	15.5%	8.4%	184%
R	32	20.6%	6.3%	328%
M	4	2.6%	1.5%	171%
W	3	1.8%	1.2%	168%
P	14	9.0%	6.2%	145%
N	7	4.5%	3.3%	135%
F	6	3.9%	3.2%	122%
K	10	6.5%	6.0%	107%
G	11	7.1%	6.6%	107%
L	12	7.7%	8.5%	91%
H	3	1.9%	2.7%	71%
V	5	3.2%	5.3%	61%
D	5	3.2%	5.5%	58%
Q	3	1.9%	4.6%	42%
C	1	0.6%	1.8%	36%
I	1	0.6%	2.1%	31%
T	2	1.3%	4.7%	27%
S	3	1.9%	7.8%	25%
E	4	2.6%	11.5%	22%
Y	0	0.0%	2.6%	0%
PrecursorStart	5	3.2%		

Fig. 14a

AminoAcid after First Cleavage				
		% Cleavage	% Present	Δ
S	26	16.8%	7.8%	214%
D	18	11.6%	5.5%	210%
V	13	8.4%	5.3%	158%
H	6	3.9%	2.7%	143%
G	14	9.0%	6.8%	136%
M	3	1.9%	1.5%	128%
I	4	2.6%	2.1%	124%
A	16	10.3%	8.4%	122%
K	9	5.8%	6.0%	97%
P	9	5.8%	6.2%	93%
Q	6	3.9%	4.6%	84%
L	11	7.1%	8.5%	83%
T	6	3.9%	4.7%	82%
N	3	1.9%	3.3%	58%
Y	2	1.3%	2.6%	50%
C	1	0.6%	1.8%	36%
E	5	3.2%	11.5%	28%
R	2	1.3%	6.3%	21%
F	1	0.6%	3.2%	20%
W	0	0.0%	1.2%	0%

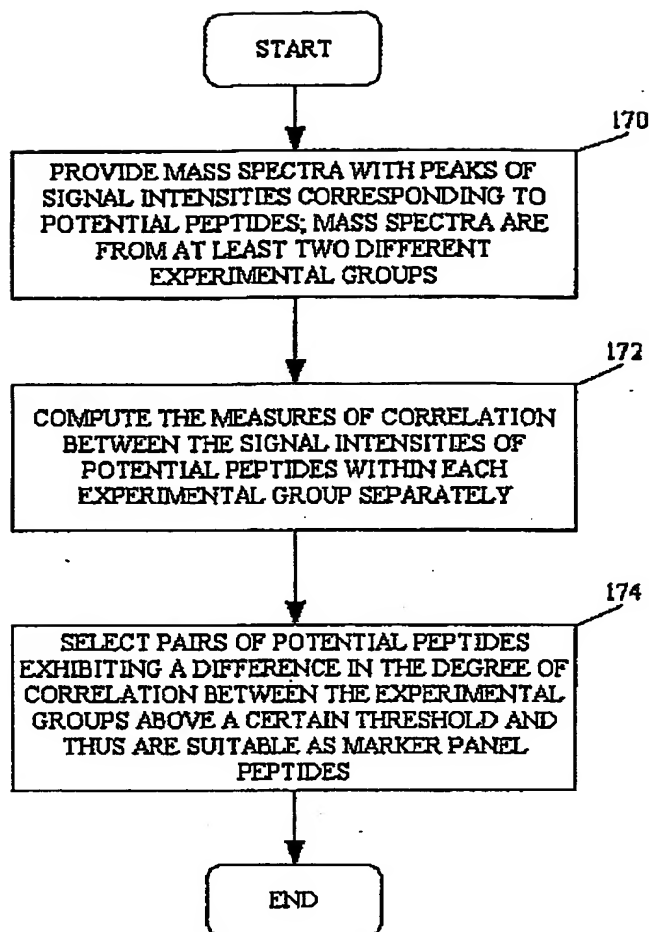
Fig. 14b

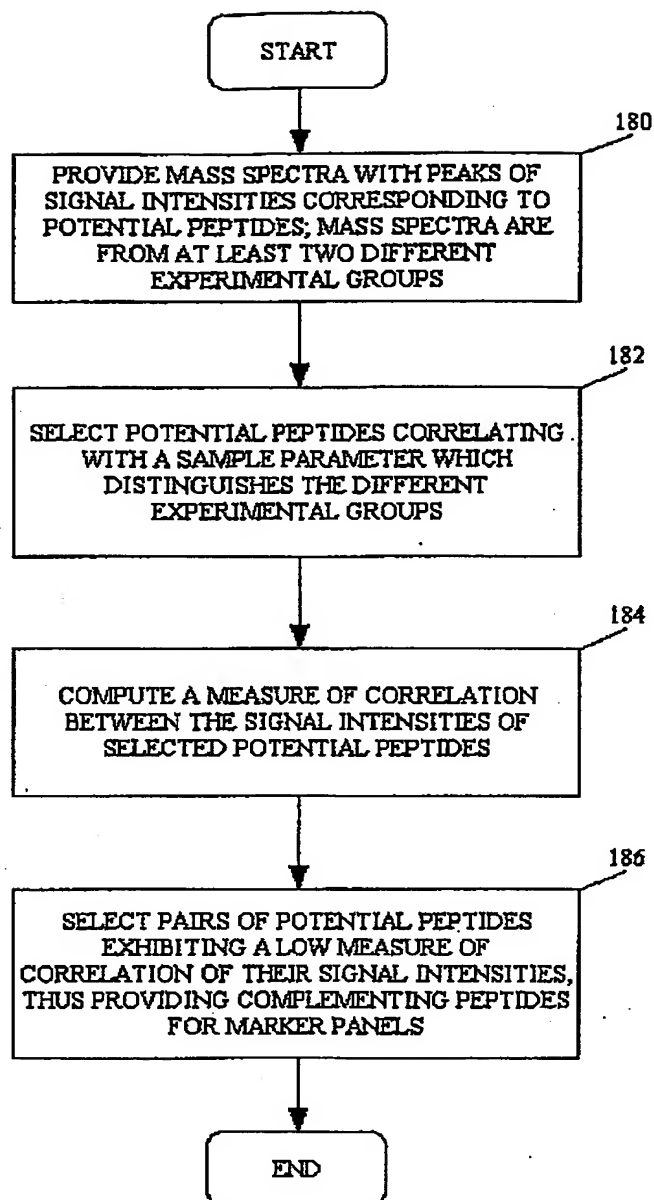
AminoAcid Before Last Cleavage				
		% Cleavage	% Present	Δ
R	26	16.8%	6.3%	267%
E	28	18.7%	11.5%	162%
N	7	4.5%	3.3%	135%
D	11	7.1%	5.5%	128%
A	16	10.3%	8.4%	122%
Q	8	5.2%	4.6%	111%
R	10	6.5%	6.3%	103%
F	5	3.2%	3.2%	102%
L	13	8.4%	8.5%	98%
G	10	6.5%	6.6%	97%
K	8	5.8%	6.0%	97%
M	2	1.3%	1.5%	85%
T	6	3.9%	4.7%	82%
S	9	5.8%	7.8%	74%
C	2	1.3%	1.8%	72%
V	5	3.2%	5.3%	61%
Y	2	1.3%	2.6%	50%
H	2	1.3%	2.7%	48%
P	2	1.3%	6.2%	21%
I	0	0.0%	2.1%	0%

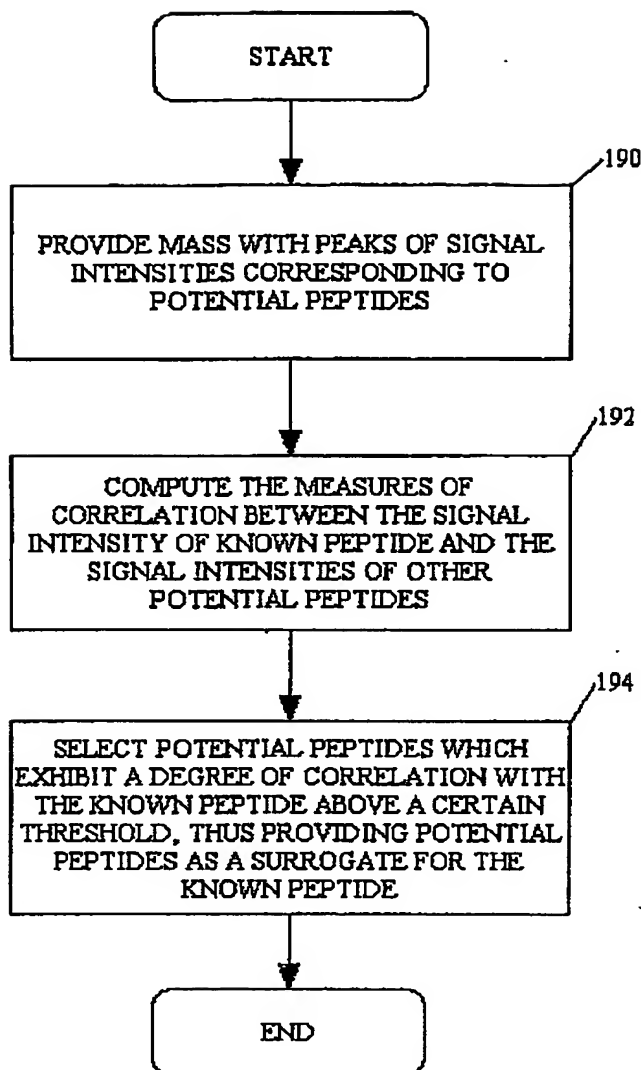
Fig. 14c

AminoAcid After Last Cleavage				
		% Cleavage	% Present	Δ
Precursor end	30	19.4%		
R	26	16.8%	6.3%	267%
K	19	12.3%	6.0%	204%
W	3	1.9%	1.2%	168%
F	8	5.2%	3.2%	162%
G	12	7.7%	6.6%	117%
V	9	5.8%	5.3%	110%
T	7	4.5%	4.7%	96%
I	2	1.3%	2.1%	62%
A	7	4.5%	8.4%	54%
P	5	3.2%	6.2%	52%
Y	2	1.3%	2.6%	50%
M	1	0.6%	1.5%	43%
Q	3	1.9%	4.8%	42%
S	5	3.2%	7.8%	41%
N	2	1.3%	3.3%	39%
L	5	3.2%	8.5%	38%
D	3	1.9%	5.5%	35%
E	6	3.9%	11.5%	34%
C	0	0.0%	1.8%	0%
H	0	0.0%	2.7%	0%

Fig. 14d

**Fig. 15**

**Fig. 16**

**Fig. 17**

Case No.	Fraction 54 m/z 2743.0	Fraction 54 m/z 1371.5	Fraction 56 m/z 2927.2	Fraction 20 m/z 11143
	k=20	k=19	k=16		k=19	
1	21648	712	2620		1452	
2	1830	1320	1199		2554	
3	21353	2022	3159		2139	
4	24223	2454	2431		2169	
5	3725	2719	982		1038	
6	13548	2956	1689		1300	
7	16606	3260	1402		2213	
8	20902	3435	624		887	
9	10321	3444	427		2145	
10	31047	3498	2238		1516	
11	31142	3592	4405		1255	
12	37241	3745	2785		1739	
13	22656	3822	2264		2576	
14	24366	3852	1752		1139	
15	16638	3935	1147		2182	
16	37171	4092	2393		1069	
17	33188	4115	1578		1681	
18	27596	4127	3228		1463	
19	39668	4348	3604		318	
20	12983	4362	1048		3039	
21	14420	4488	899		2676	
22	23261	4634	1965		3071	
23	30507	4710	2715		1247	
24	41494	4928	5343		1238	
25	36664	5107	3914		3156	
26	42465	5135	2729		1768	
27	42551	5135	3010		2500	
28	35473	5201	2242		1978	
29	48611	5906	2381		1075	
30	28413	5914	1855		3189	
31	35258	5954	3368		2140	
32	44774	6056	4167		670	
33	46137	6465	7640		1719	
34	40892	6531	1630		1241	
35	48202	7076	11222		3826	
36	43760	7183	4771		1565	
37	50211	7316	5443		2060	

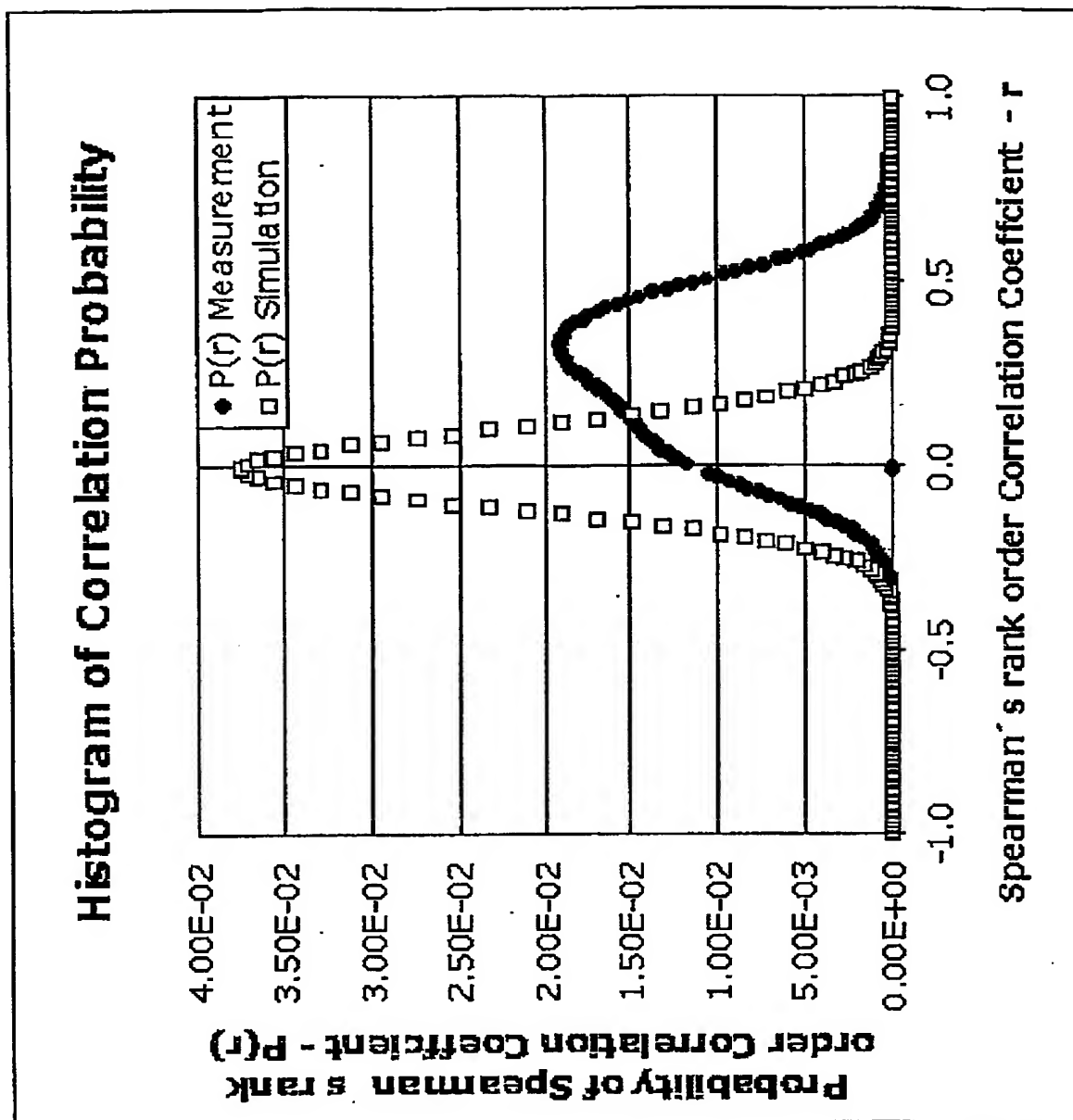
Fig. 18a

Case No.	Fraction 54 m/z 2743.0	Fraction 54 m/z 1371.5	Fraction 56 m/z 2927.2 ...	Fraction 20 m/z 1114.3 ...
38	49824	7410	3004	1113
39	50785	7752	6412	1616
40	46200	7821	3689	3725
41	52471	7949	5395	1837
42	49299	8280	4623	1207
43	45032	8483	4881	1566
44	51224	8562	6481	2194
45	51901	8638	10081	2047
46	51084	8776	14193	1478
47	50928	8852	6635	287
48	50707	10097	8877	1458
49	52304	10259	6244	1860
50	48355	10661	5195	3695
51	51363	10685	11403	1261
52	54423	10846	11299	2067
53	55167	11041	12868	1545
54	55091	11539	5597	2381
55	56825	11912	7718	2409
56	53173	12022	8865	1969
57	51649	12057	7855	1295
58	51328	12095	9035	2043
59	53464	12641	6408	856
60	54542	12891	10363	1858
61	56950	13172	7586	1802
62	43273	14559	20080	596
63	57335	14922	12288	2916
64	55118	14997	10078	1761
65	57147	16164	7726	2626
66	55584	16216	17106	2623
67	59414	16550	15122	539
68	57093	16689	19689	2078
69	57841	18254	16079	1659
70	54084	18734	19524	395
71	56325	22730	10828	2326
72	58386	24159	16681	1631
73	54843	26671	44356	3183
74	53935	27937	30189	1403

Fig. 18b

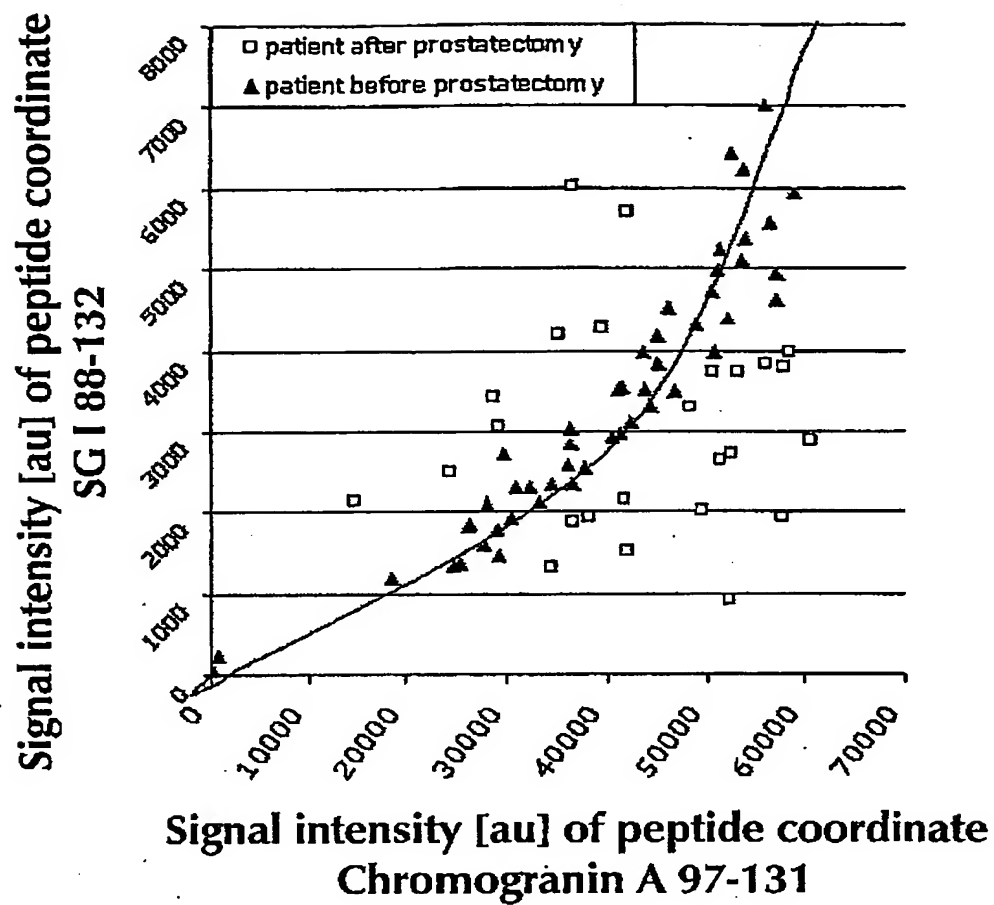
	Fraction 54 m/z 2743.0 and ...		
Measure of Association	Fraction 54 m/z 1371.5	Fraction 56 m/ 2927.2	Fraction 20 m/z 1114.3
Spearman's rank order correlation	0.9298	0.8761	-0.0044
Pearson's product moment correlation	0.7318	0.5855	-0.0781
Kendall's rank correlation tau	0.7704	0.6919	0.0107
MST diameter	50	40	29

Fig. 19

**Fig. 20**

Hub - Pept ide	Corre- lation	Related peptide	Relative Mono- isotopic mass [Da]	Amino Acid Sequence
Chromogranin A 97 - 131			3905.764	HSGF EDELSEVLEN QSSQAELKEA VEEPSSKDVM E
	r=0.67	Secretogranin I 88-132	4605.025	DPADASEAHESSSRGEAGAP GEEDIQGPTKADTEKWAEGG GHSRE
	r=0.71	Secretogranin II 529-566	4152.921	G QGSSEDDLQEE EQIEQAIKEH LNQGSSQETD KLAPVS
	r=0.72	Secretogranin V 181-202	2448.334	SVNPYLQGQRLDNVVARKSV PH

Fig. 21

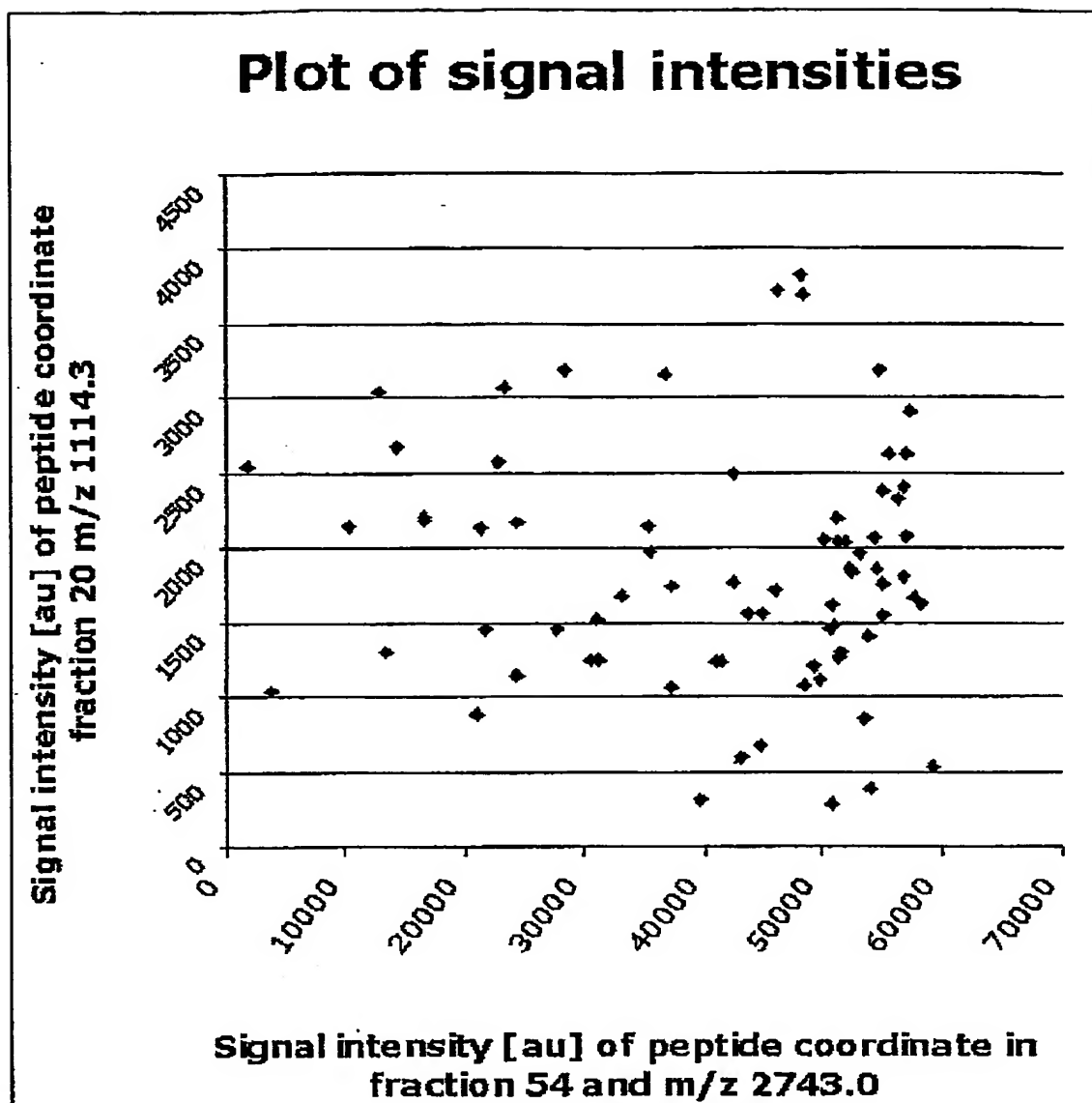
**Fig. 22**

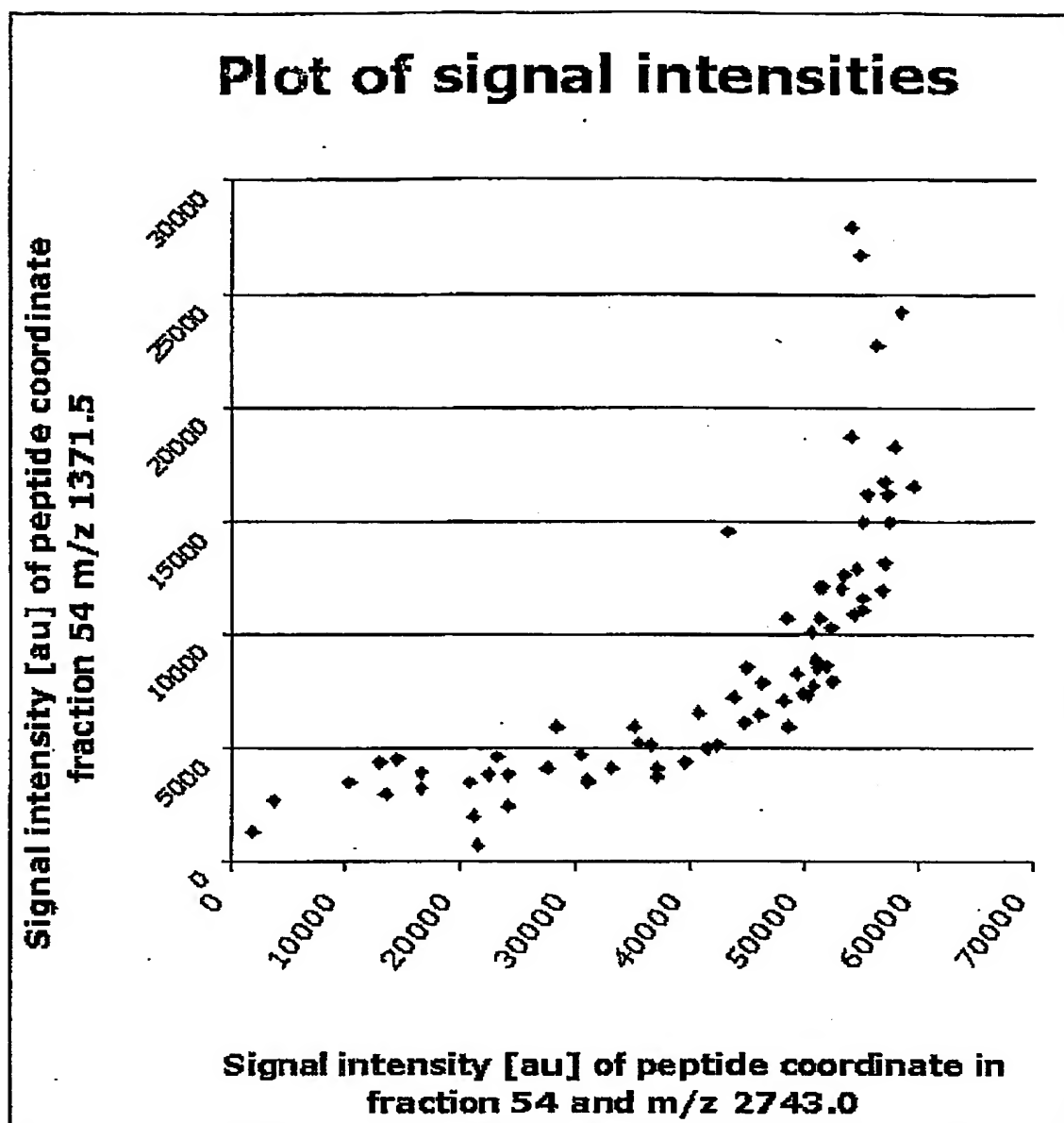
	Fraction 54 m/z	Fraction 54 m/z	Fraction 56 m/z	Fraction 20 m/z
	2743.8	1371.5	2927.2		1114.3	
	k=0	k=1	k=2		k=19	
case 1	21648	3747	7051		1452	
case 2	1838	4355	5630		2554	
case 3	21953	5057	7590		2139	
case 4	24223	5489	6862		2169	
case 5	3725	5754	5413		1038	
case 6	13548	5991	6120		1300	
case 7	16686	6295	5833		2213	
case 8	28982	6470	5055		887	
case 9	19321	6479	4858		2145	
case 10	31047	6533	6609		1516	
case 11	34142	6627	8836		1255	
case 12	37241	6780	7216		1739	
case 13	22656	6857	6695		2576	
case 14	24366	6887	6183		1139	
case 15	16628	6970	5578		2182	
case 16	37171	7127	6824		1069	
case 17	33188	7150	6009		1681	
case 18	27596	7162	7639		1463	
case 19	39668	7383	8035		318	
case 20	12983	7397	5479		3039	
case 21	14420	7523	5330		2676	
case 22	23261	7669	6396		3071	
case 23	38587	7745	7146		1247	
case 24	41494	7963	9774		1238	
case 25	36664	8142	8345		3156	
case 26	42465	8170	7160		1768	
case 27	42551	8170	7441		2500	
case 28	35473	8236	6673		1978	
case 29	48611	8941	6812		1075	
case 30	28413	8949	6286		3189	
case 31	35258	8989	7799		2140	
case 32	44774	9091	8598		670	
case 33	46127	9500	12071		1719	
case 34	40892	9566	6061		1241	
case 35	48202	10111	15653		3826	
case 36	43768	10218	9202		1565	

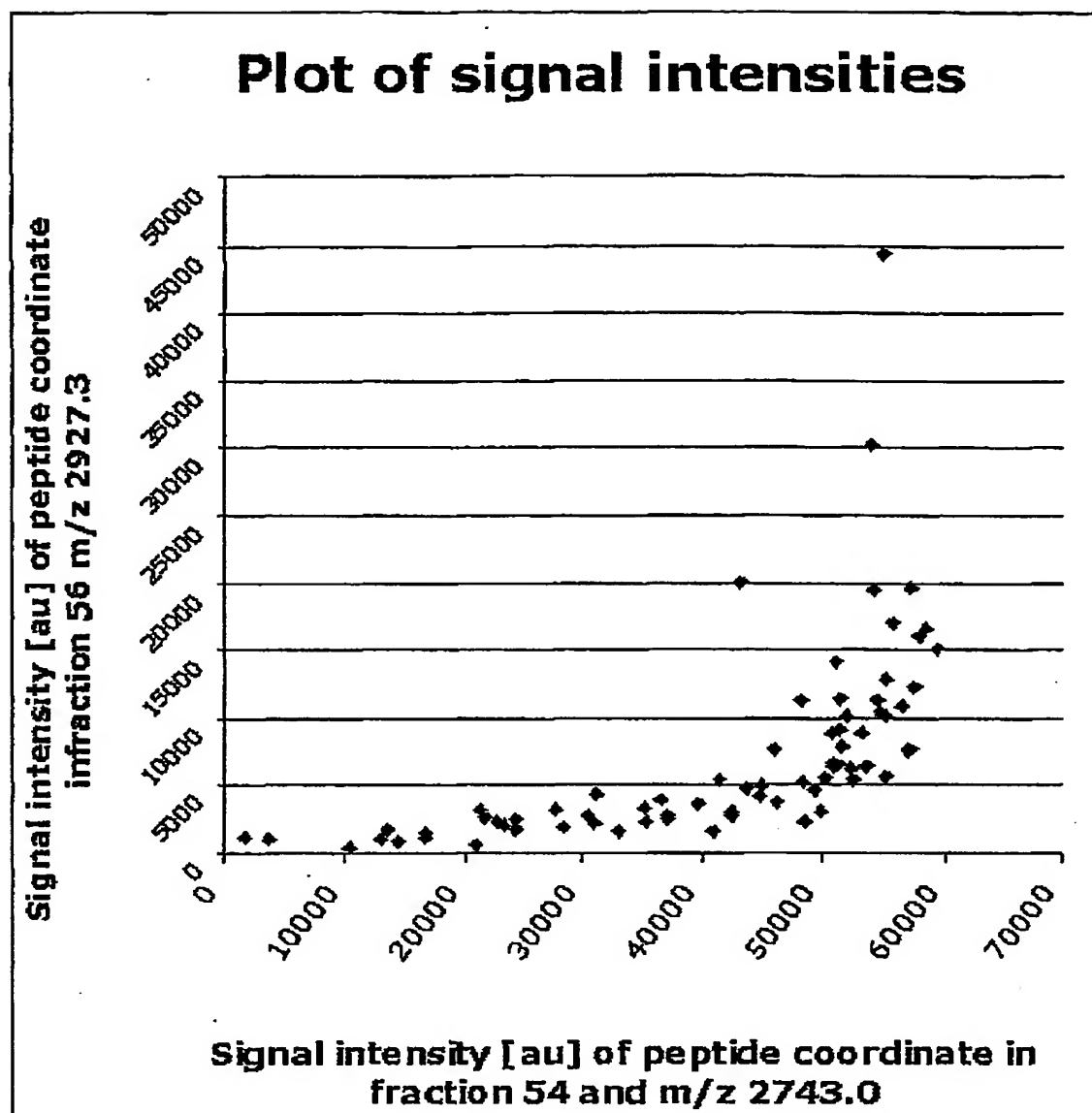
Fig. 23a

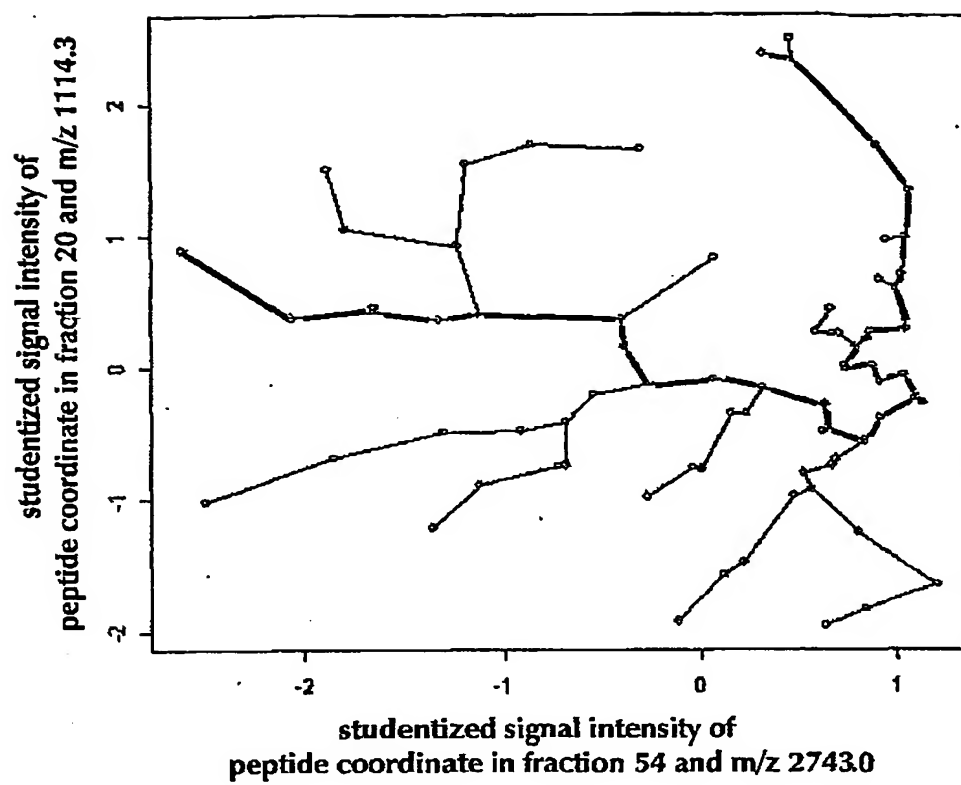
	Fraction 54 m/z 2743.0	Fraction 54 m/z 1371.5	Fraction 56 m/z 2927.2	Fraction 20 m/z 1114.3
case 37	5021.1	10351	9874		1113	
case 38	4982.4	10445	7435		1616	
case 39	5078.5	10787	10843		3725	
case 40	4620.8	10856	8120		1837	
case 41	5247.1	10984	9826		1207	
case 42	4029.9	11315	9054		1566	
case 43	4503.2	11518	9312		2194	
case 44	5123.4	11597	10912		2047	
case 45	5150.1	11673	14512		1478	
case 46	5108.4	11811	18624		287	
case 47	5092.8	11887	11066		1458	
case 48	5070.7	13132	13308		1860	
case 49	5230.4	13294	10675		3695	
case 50	4835.5	13696	9626		1261	
case 51	5136.3	13720	15834		2067	
case 52	5442.3	13881	15730		1545	
case 53	5516.7	14076	17299		2381	
case 54	5509.1	14574	10028		2409	
case 55	5683.5	14947	12149		1969	
case 56	5347.3	15057	13296		1295	
case 57	5164.9	15092	12286		2043	
case 58	5132.8	15130	13466		856	
case 59	5345.4	15676	10839		1858	
case 60	5454.2	15926	14794		1802	
case 61	5695.0	16207	12017		596	
case 62	4327.3	17594	24511		2916	
case 63	5733.5	17957	16719		1761	
case 64	5511.8	18032	14509		2626	
case 65	5714.7	19199	12157		2623	
case 66	5558.4	19251	21537		539	
case 67	5941.4	19585	19553		2078	
case 68	5709.3	19724	24120		1659	
case 69	5784.1	21289	20510		395	
case 70	5408.4	21769	23955		2326	
case 71	5632.5	25765	15259		1631	
case 72	5838.6	27194	21112		3183	
case 73	5484.3	29706	48787		1403	
case 74	5393.5	30972	34620		1113	

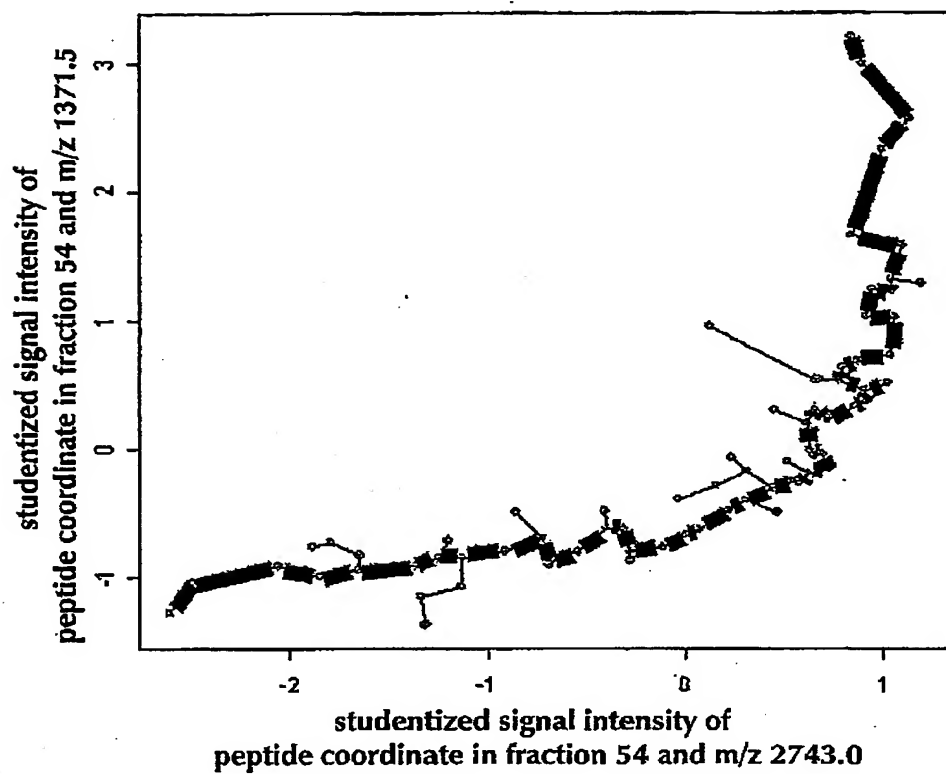
Fig. 23b

**Fig. 24a**

**Fig. 24b**

**Fig. 24c**

**Fig. 25a**

**Fig. 25b**

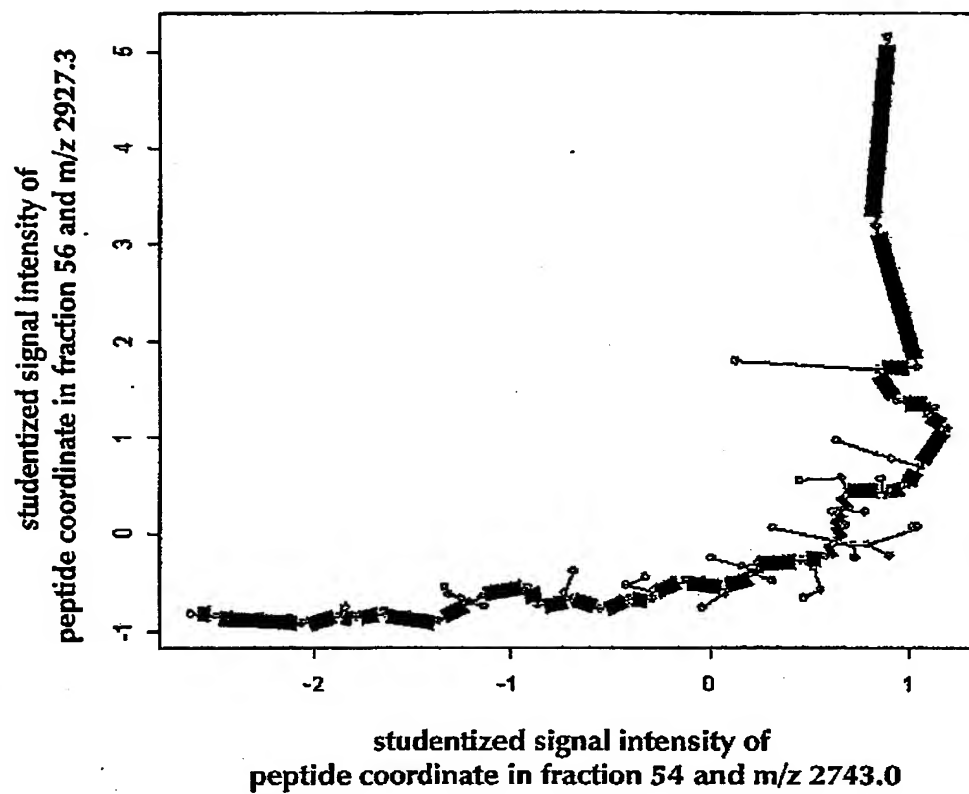


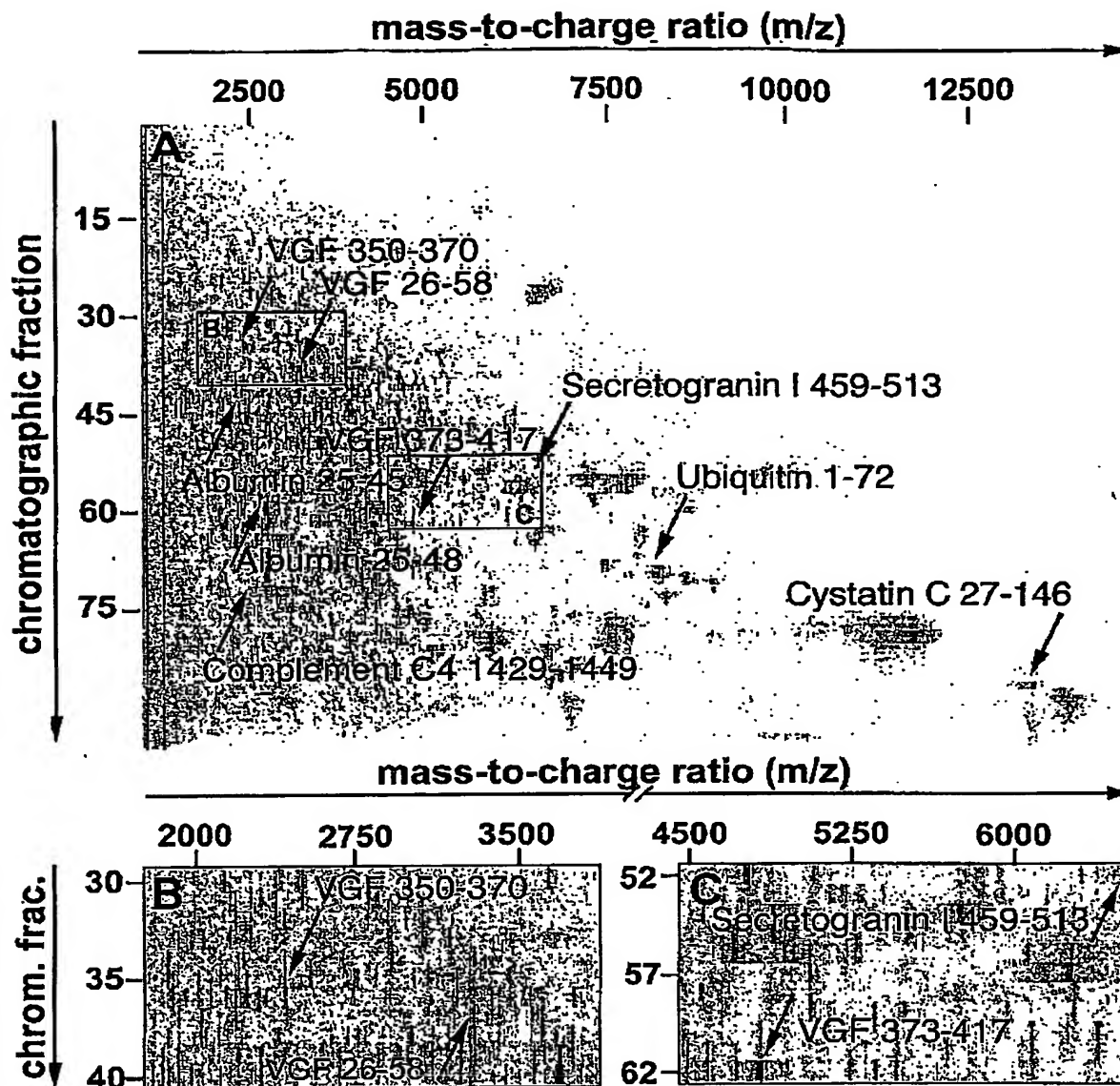
Fig. 25c

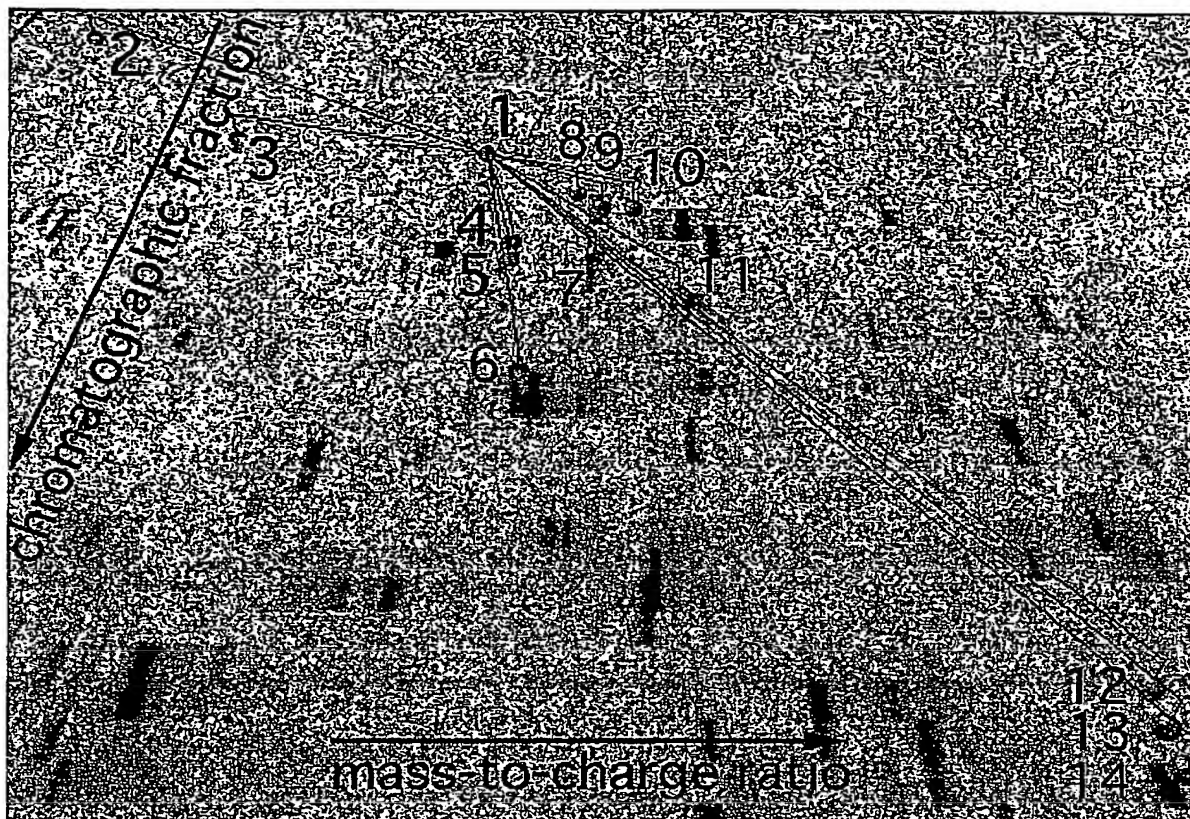
m/z	n			
	1	2	3	4
1371.5	-1371.5	0.0	1371.5	2743.0
2927.3	183.3	3109.6	6035.9	8962.2

Fig. 26

1	10	20	30	40
MKWVTFISLL FLFSSAYSRG VFRR <u>DAHKSE VAHRTYDLGE</u>				
	50	60	70	80
<u>ENFKALVLIA</u> KREAQYLQQC PFEDHVKLVN EVTEFAKTCV				
	90	100	110	120
ADESAENCDK SLHTLFGDKL CTVATLRETY GEMADCCAKQ				
	130	140	150	160
EPERNECFLQ HKDDNPNLPR LVRPEVDVMC TAFHDNEETF				
	170	180	190	200
LKKYLYEIAR RHPYFYAPEL LFFAKRYKAA FTECCQAADK				
	210	220	230	238
AACLLPKLDE LRDEGKASSA KQRLKCASLQ KFGERAFFK				

Fig. 27

**Fig. 28**

**Fig. 29**

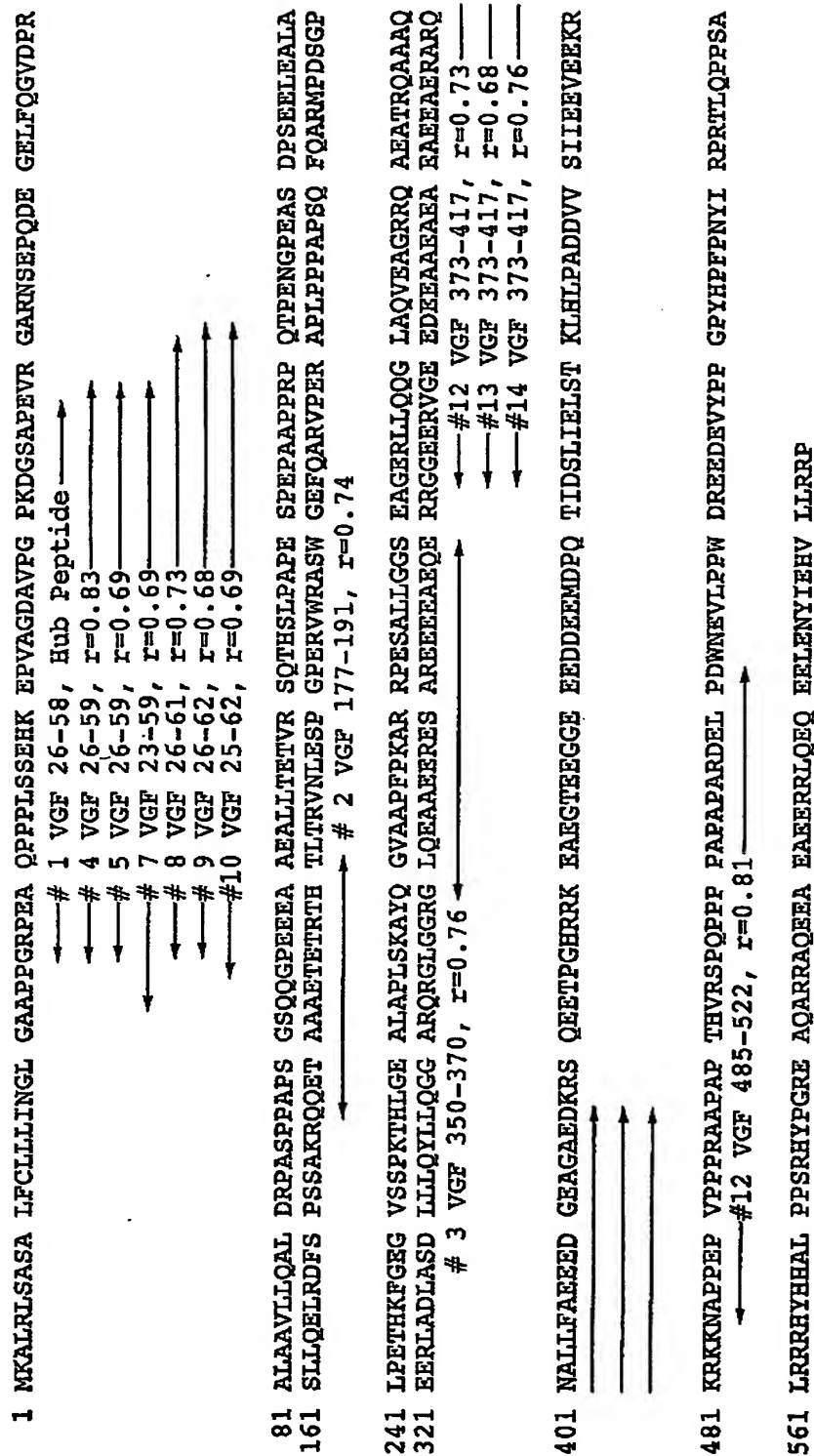


Fig. 30

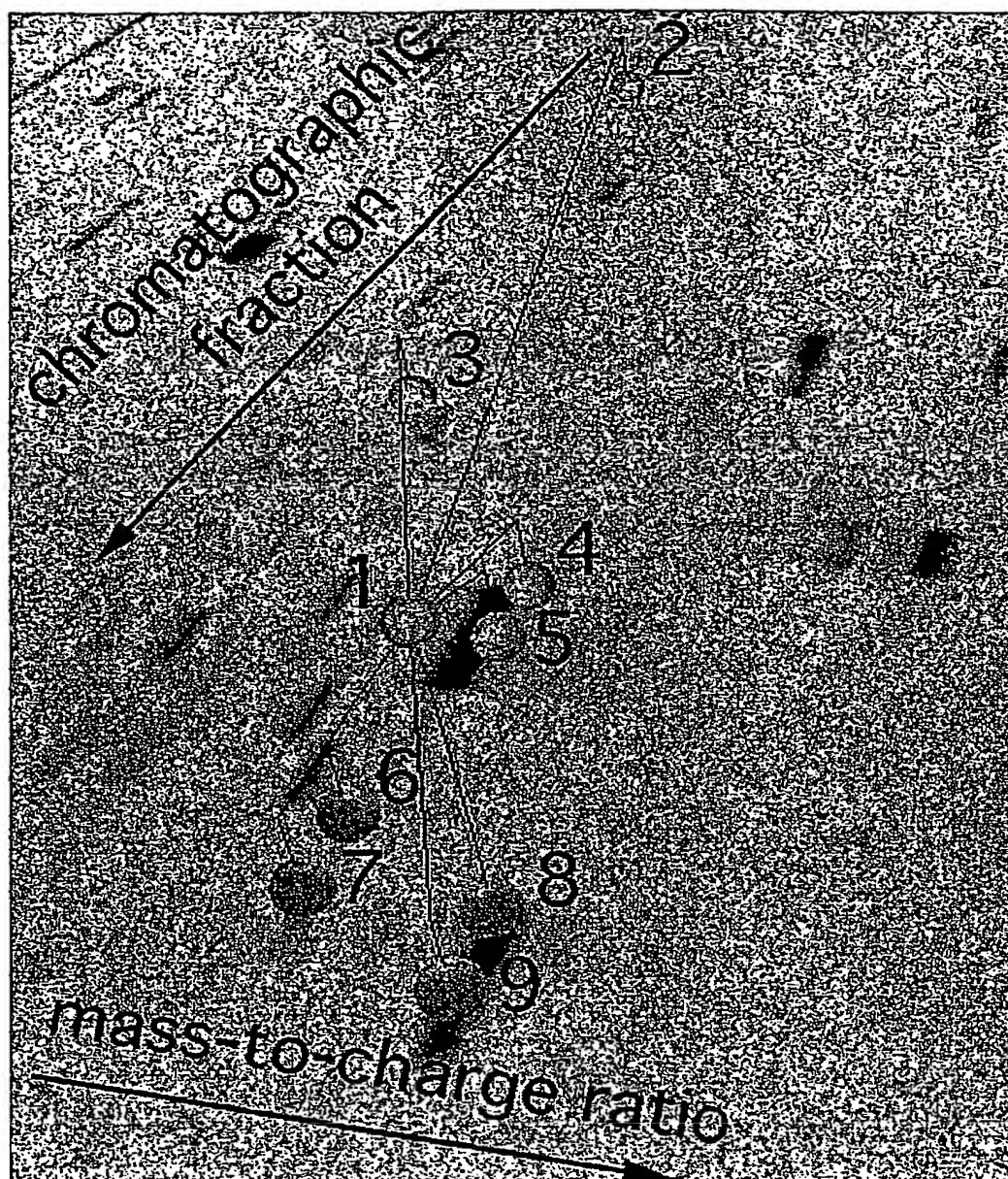
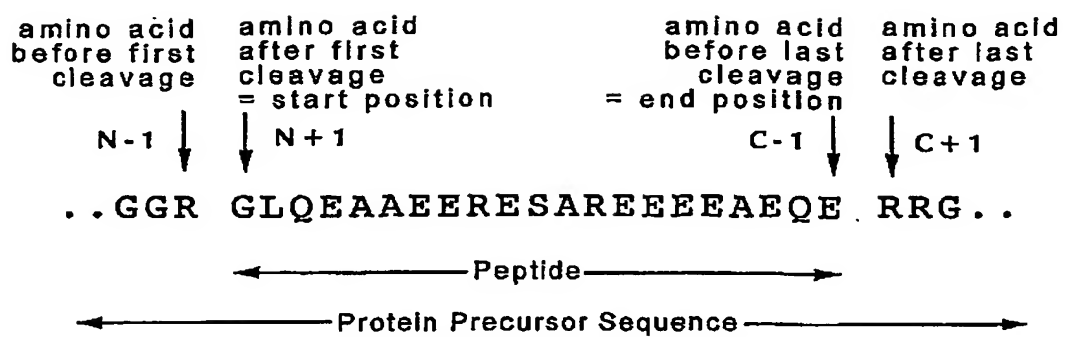


Fig. 31

$ r \geq$	Number of ...			Percentage of Correct Predictions
	Correct Precursor Predictions	False Precursor Predictions	All Predictions	
0.95	18	0	18	100%
0.90	40	4	44	91%
0.85	58	10	68	85%
0.80	104	26	130	80%
0.75	178	76	256	70%
0.70	314	192	506	62%
0.65	512	456	968	53%
0.60	756	990	1746	43%
0.55	964	1872	2836	34%
0.50	1186	3086	4272	28%

Fig. 32

**Fig. 33**

	Number and Percentage of Amino Acid Found at Position of Interest									x-fold Change of Percentages of Amino Acid Compared to General Occurrence			
Amino Acid	n(N-1)		n(N+1)		n(C-1)		n(C+1)		n (Any position)	x(N-1)	x(N+1)	x(C-1)	x(C+1)
A	16	12%	18	13%	16	12%	5	5%	5612 8.2%	1.4	1.6	1.4	0.6
C	1	1%	1	1%	2	1%	0	0%	1109 1.6%	0.4	0.4	0.9	0.0
D	5	4%	22	16%	8	6%	4	4%	3994 5.8%	0.6	2.8	1.0	0.6
E	4	3%	5	4%	30	22%	3	3%	8069 11.8%	0.2	0.3	1.8	0.2
F	5	4%	4	3%	3	2%	7	7%	2195 3.2%	1.1	0.9	0.7	2.0
G	6	4%	12	9%	7	5%	7	7%	4171 6.1%	0.7	1.4	0.8	1.1
H	3	2%	4	3%	2	1%	1	1%	1955 2.9%	0.8	1.0	0.5	0.3
I	0	0%	1	1%	3	2%	2	2%	1592 2.3%	0.0	0.3	0.9	0.8
K	7	5%	8	6%	12	9%	22	21%	4235 6.2%	0.8	0.9	1.4	3.4
L	9	7%	11	8%	10	7%	8	8%	5982 8.7%	0.7	0.9	0.8	0.9
M	5	4%	5	4%	0	0%	0	0%	1120 1.6%	2.2	2.2	0.0	0.0
N	4	3%	4	3%	8	6%	0	0%	2365 3.5%	0.8	0.8	1.7	0.0
P	15	11%	9	6%	1	1%	1	1%	4310 6.3%	1.7	1.0	0.1	0.1
Q	0	0%	7	5%	5	4%	3	3%	3334 4.9%	0.0	1.0	0.7	0.6
R	42	31%	0	0%	9	6%	28	27%	4142 6.0%	5.1	0.0	1.1	4.4
S	4	3%	20	14%	10	7%	3	3%	5154 7.5%	0.4	1.9	1.0	0.4
T	4	3%	3	2%	4	3%	3	3%	3150 4.6%	0.6	0.5	0.6	0.6
V	5	4%	3	2%	6	4%	5	5%	3581 5.2%	0.7	0.4	0.8	0.9
W	1	1%	2	1%	1	1%	3	3%	720 1.1%	0.7	1.4	0.7	2.7
Y	0	0%	0	0%	2	1%	0	0%	1726 2.5%	0.0	0.0	0.6	0.0
Sum	136	100 %	139	100 %	139	100%	105	100%	68516 100%				

Fig. 34

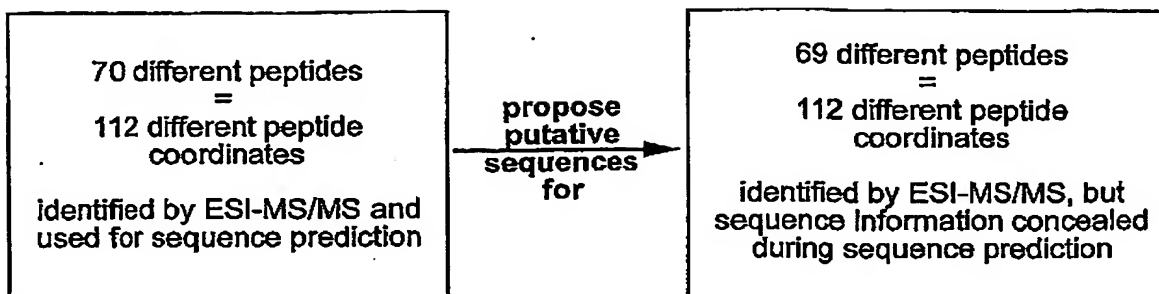
Pair of Amino Acids ...		# of Peptides	% of Peptides	# of Amino Acid pairs in all Precursors	% of Amino Acid pairs in all Precursors	x-fold Increase
... Before Amino-Terminal Cleavage	RR	18	12.9%	398	0.58%	22.2
	KR	13	9.4%	351	0.51%	18.2
... After Amino-Terminal Cleavage	DA	15	10.8%	170	0.25%	43.4
	GR	5	3.6%	215	0.31%	11.4
... Before Carboxy-Terminal Cleavage	QK	7	5.0%	169	0.25%	20.4
	VN	6	4.3%	188	0.27%	15.7
	GA	6	4.3%	293	0.43%	10.1
... After Carboxy-Terminal Cleavage	KR	16	11.5%	351	0.51%	22.4

Fig. 35

Hub peptide VGF 26-58

- | |
|--|
| <ul style="list-style-type: none">* predicts unknown peptide with $m/z = 3688.03$ as VGF 26-62<ul style="list-style-type: none">+ calculated m/z matches found m/z (prerequisite condition)+ same start position as hub peptide (+ 69 bonus points)+ R as amino acid after end position (+ 4 bonus points)* predicts unknown peptide with $m/z = 2419.41$ as VGF 350-370<ul style="list-style-type: none">+ calculated m/z matches found m/z (prerequisite condition)+ R as amino acid before start position (+ 5 bonus points)+ RR as amino acids before start position (+22 bonus points) |
|--|

Fig. 36

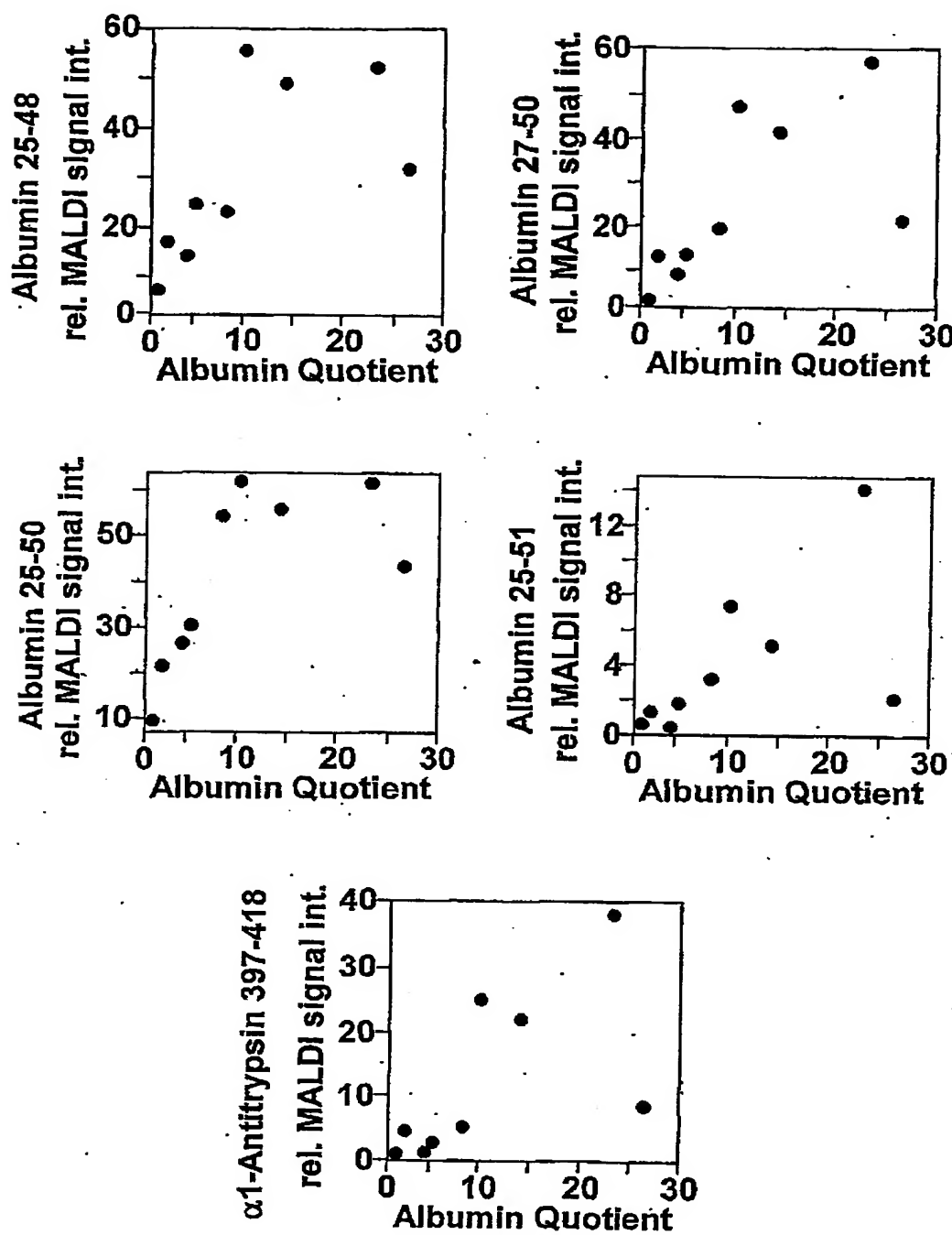
**Fig. 37**

$ r \geq 0.75$	Any proposal			Proposal With Most Bonus Points		
	Precursor Correct Start- or End Position Correct	Precursor Correct Start- or End Position False	Precursor False Start- or End Position False	Precursor Correct Start- or End Position Correct	Precursor Correct Start- or End Position False	Precursor False Start- or End Position False
Model 1: No rules	5 6%	61 75%	15 19%	3 11%	19 70%	5 19%
Model 2: Only Rules Considering Single Amino Acids at Cleavage Sites	13 16%	58 72%	10 12%	10 37%	14 52%	3 11%
Model 3: Only Rules Considering Pairs of Amino Acid Pairs	18 22%	54 67%	11 14%	15 56%	9 33%	3 11%
Model 4: Only Rules Considering Common Start- or End Position	17 21%	51 63%	13 16%	13 48%	11 41%	3 11%
Model 5: Combination: Only Rules Considering Single Amino Acids & Pairs of Amino Acid	19 23%	54 67%	8 10%	18 67%	6 22%	3 11%
Model 6: Combination: all rules	28 35%	45 56%	8 10%	23 85%	1 4%	3 11%

Fig. 38

Correlation to:		Hub:	Monoisotop. Mass	Sequence
Albumin	Alb. 25-48			
r=0.73		Albumin 25-48	2752.4	DAHKSEVAHRFKDLGEENFKALVL
related Peptide to Alb. 25-48:				
r=0.80	r=0.77	Albumin 27-50	2750.5	HKSEVAHRFKDLGEENFKALVLIA
r=0.76	r=0.75	Albumin 25-50	2936.6	DAHKSEVAHRFKDLGEENFKALVLIA
r=0.76	r=0.75	Albumin 25-51	3085.5	DAHKSEVAHRFKDLGEENFKALVLIAF
r=0.83	r=0.75	alpha-1- Antitrypsin 397-418	2502.3	LMIEQNTKSPLFMGKVNPTQK

Fig. 39

**Fig. 40**

**This Page is Inserted by IFW Indexing and Scanning
Operations and is not part of the Official Record**

BEST AVAILABLE IMAGES

Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images include but are not limited to the items checked:

- ☐ BLACK BORDERS
- ☐ IMAGE CUT OFF AT TOP, BOTTOM OR SIDES
- ☐ FADED TEXT OR DRAWING
- ☐ BLURRED OR ILLEGIBLE TEXT OR DRAWING
- ☐ SKEWED/SLANTED IMAGES
- ☒ COLOR OR BLACK AND WHITE PHOTOGRAPHS
- ☐ GRAY SCALE DOCUMENTS
- ☒ LINES OR MARKS ON ORIGINAL DOCUMENT
- ☐ REFERENCE(S) OR EXHIBIT(S) SUBMITTED ARE POOR QUALITY
- ☐ OTHER: _____

IMAGES ARE BEST AVAILABLE COPY.

As rescanning these documents will not correct the image problems checked, please do not report these problems to the IFW Image Problem Mailbox.